



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Golstein, Pierre
Rouvier, Eric
Fossiez, Francois
Lebecque, Serge J.E.
Djossou, Odile
Banchereau, Jacques
- (ii) TITLE OF INVENTION: Purified Mammalian CTLA-8 Antigens and Related Reagents
- (iii) NUMBER OF SEQUENCES: 10
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Townsend and Townsend and Crew LLP
 - (B) STREET: Two Embarcadero Center, Eighth Floor
 - (C) CITY: San Francisco
 - (D) STATE: California
 - (E) COUNTRY: USA
 - (F) ZIP: 94111-3834
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 09/929,612
 - (B) FILING DATE: 13-AUG-2001
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/077,203
 - (B) FILING DATE: 14-JUN-1993
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/177,747
 - (B) FILING DATE: 05-JAN-1994
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/250,846
 - (B) FILING DATE: 27-MAY-1994
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/432,994
 - (B) FILING DATE: 02-MAY-1995
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/432,994
 - (B) FILING DATE: 22-JUN-1998
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Weber, Kenneth A.
 - (B) REGISTRATION NUMBER: 31,677
 - (C) REFERENCE/DOCKET NUMBER: 015631-003115US

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1080 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 12..464

(D) OTHER INFORMATION: /product= "mouse/rat CTLA-8"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GAATTCCATC C ATG TGC CTG ATG CTG TTG CTG CTA CTG AAC CTG GAG GCT	50
Met Cys Leu Met Leu Leu Leu Leu Leu Leu Glu Ala	
1 5 10	
ACA GTG AAG GCA GCG GTA CTC ATC CCT CAA AGT TCA GTG TGT CCA AAC	98
Thr Val Lys Ala Ala Val Leu Ile Pro Gln Ser Ser Val Cys Pro Asn	
15 20 25	
GCC GAG GCC AAT AAC TTT CTC CAG AAC GTG AAG GTC AAC CTG AAA GTC	146
Ala Glu Ala Asn Asn Phe Leu Gln Asn Val Lys Val Asn Leu Lys Val	
30 35 40 45	
ATC AAC TCC CTT AGC TCA AAA GCG AGC TCC AGA AGG CCC TCA GAC TAC	194
Ile Asn Ser Leu Ser Ser Lys Ala Ser Ser Arg Arg Pro Ser Asp Tyr	
50 55 60	
CTC AAC CGT TCC ACT TCA CCC TGG ACT CTG AGC CGC AAT GAG GAC CCT	242
Leu Asn Arg Ser Thr Ser Pro Trp Thr Leu Ser Arg Asn Glu Asp Pro	
65 70 75	
GAT AGA TAT CCT TCT GTG ATC TGG GAG GCA CAG TGC CGC CAC CAG CGC	290
Asp Arg Tyr Pro Ser Val Ile Trp Glu Ala Gln Cys Arg His Gln Arg	
80 85 90	
TGT GTC AAC GCT GAG GGG AAG TTG GAC CAC CAC ATG AAT TCT GTT CTC	338
Cys Val Asn Ala Glu Gly Lys Leu Asp His His Met Asn Ser Val Leu	
95 100 105	
ATC CAG CAA GAG ATC CTG GTC CTG AAG AGG GAG CCT GAG AAG TGC CCC	386
Ile Gln Gln Glu Ile Leu Val Leu Lys Arg Glu Pro Glu Lys Cys Pro	
110 115 120 125	
TTC ACT TTC CGG GTG GAG AAG ATG CTG GTG GGC GTG GGC TGC ACC TGC	434
Phe Thr Phe Arg Val Glu Lys Met Leu Val Gly Val Gly Cys Thr Cys	
130 135 140	

GTT TCC TCT ATT GTC CGC CAT GCG TCC TAAACAGAGA CCTGAGGCTA 481
 Val Ser Ser Ile Val Arg His Ala Ser
 145 150

GCCCCCTAAGA AACCCCTGCG TTTCTCTGCA AACTTCCTTG TCTTTTTTAAA ACAGTTCACA 541
 GTTGAATCTC AGCAAGTGAT ATGGATTAA AGGCGGGGTT AGAATTGTCT GCCTTCCACC 601
 CTGAAAAGAA GGCGCAGAGG GGATATAAAT TGCTTCTTGT TTTTCTGTGG GCTTTAAATT 661
 ATTTATGTAT TTA CTCTATC CCGAGATAAC TTTGAGGCAT AAGTTATTTT AATGAATTAT 721
 CTACATTATT ATTATGTTTC TTAATGCAGA AGACAAAATT CAAGACTAAG AAATTTTATT 781
 ATTTAAAAGG TAAAACCTAT ATTTATATGA GCTATTTATG GGTCTATTTA TTTTCTTCA 841
 GTGCTAAGAT CATGATTATC AGATCTACCT AAGGAAGTCC TAAATAATAT TAAATATTAA 901
 TTGAAATTTT AGTTTTACTA TTTGCTTATT TAAGGTTCCC TCCTCTGAAT GGTGTGAAAT 961
 CAAACCTCGT TTTATGTTTT TAAATTATTG AGGCTTCGAA AAATTGGGCA ATTTAGCTTC 1021
 CTACTGTGTG TTTAAAACC TTGTAACAAT ATCACTATAA TAAATTTTGT GAAGAAAAT 1080

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Cys Leu Met Leu Leu Leu Leu Leu Asn Leu Glu Ala Thr Val Lys
 1 5 10 15

Ala Ala Val Leu Ile Pro Gln Ser Ser Val Cys Pro Asn Ala Glu Ala
 20 25 30

Asn Asn Phe Leu Gln Asn Val Lys Val Asn Leu Lys Val Ile Asn Ser
 35 40 45

Leu Ser Ser Lys Ala Ser Ser Arg Arg Pro Ser Asp Tyr Leu Asn Arg
 50 55 60

Ser Thr Ser Pro Trp Thr Leu Ser Arg Asn Glu Asp Pro Asp Arg Tyr
 65 70 75 80

Pro Ser Val Ile Trp Glu Ala Gln Cys Arg His Gln Arg Cys Val Asn
 85 90 95

Ala Glu Gly Lys Leu Asp His His Met Asn Ser Val Leu Ile Gln Gln
 100 105 110

Glu Ile Leu Val Leu Lys Arg Glu Pro Glu Lys Cys Pro Phe Thr Phe
 115 120 125

Arg Val Glu Lys Met Leu Val Gly Val Gly Cys Thr Cys Val Ser Ser
 130 135 140

Ile Val Arg His Ala Ser
 145 150

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2520 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1574..2029
- (D) OTHER INFORMATION: /product= "Saimiriine herpesvirus 2
 immediate-early protein"
 /note= "open reading frame 2 (ORF2)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AGCTTCATGC AAATACATCT TATCTTACCA GATTCTCGCC TCATTTGCAA ACATGCCTCA	60
TCTTTTGAGA AGAAACGCAA TTCGAAC TTC TAATGCT CCTGAAGAGC AGCCTGTGCT	120
GCAGCCTGAG CTTGATGCTA TTGAAGAGCT AGAATAAGAG CTATTTTTTG ACGATGGGTG	180
CTGCCTTTCT GTTCAAGAAA TCTGCTTAAT TGTTCCTGGA TTCTTATTGT TTCTGCTAGC	240
TGTAATTGTT TTTTATAACT ATACAGACAC AGATCAATTT GTGAAGCTGA CACATCTTAT	300
GAGCCACAAA AATTCTATCA AAGGACCTTT TGATCTTTAA GGTATGTACT CATAATTTTA	360
TTTTTTTATT TCTAAAACAA TCTTAGTATA TATAATTAAT ACAAATTTTA GAAAATACTA	420
TAATAAATAT TGAAAGCTGT ATTTACATTG TAAACTATAT ATAGGCAATG TAAAGTCATT	480
CTAACTTTAG GTTTGCTTTA CCTGTTACAG AACTTCACC TGTGTGTCAA GAGCTGCAAA	540
CATGGCTTTA GACTTAAGAA ATCTTAAACA CCTGACTGCT AACTTCAGTT TTAGAATAAT	600
GATATGGATT ATGCTATGTT TGGCTCTACC TACTGATAGT AAACCTATTT CAACAACCTGA	660
AGCTCCAATA CTAAACATAA CACAATCTCC AAGTTTGAAC ATCTCATCAC CTTCTACTTT	720
AGAACCTTCA GAGCCTCTTA AAAACTGTAC AACATTCTTA GACTTACTTT GGCAGCGGCT	780
GGGCGAGAAC GCTTCTATAA AGGACTTGAT GTTAACATTA CAACGAGAAG AAGTCCACGG	840
AAGAATGACT AACTTCCTT CACCTAGACC AAGCAGTAAA GTTGAAGAAC AACAGTTACA	900
AAGACCTAGA AACTTACTGC CTA CTGCTGT CGGGCCACCT CATGTCAAAT ATAGACTATA	960
TAATCGCTTA TGGAAGCTC CTAAAGGAGC TGATGTTAAT GGTAAACCTA TACAATTTGA	1020

TGACCCTCCT CTTCTTATA CAGGGGCATA TAATGATGAT GGTGTTTTAA TGGTTAATAT	1080
TAATGGAAAA CATGTGAGGT TTGATAGCTT GTCTTATTGG GAAAGAATTA AAAGATCTGG	1140
TACCCCATGG TGTATAAAGA CACCAAGTGA AAAAGCAGCA ATATTGAAGC AGCTTTTAAA	1200
AGCTGAAAAA AAATGTAGGA CTACTTCTAA ACGTATCACT GAGTTAGAAG AGCAGATTAA	1260
AGAACTAGAA AAAACTAGTA CATCTCCATA GATTACTGTT AGAATGTGTT TATCATACTA	1320
AAATAAATGC TTTATGTATT GCAATATTAC TTGTTTGCTA TGACTTTGGT ATATGAAATG	1380
CAAATCTTAA ATAAAAAGTT TTTGTCTAGT ATTGGCGTCA CTGTATTTTA CTAGCAAAAA	1440
TATATAAATT GTTATGTAGC AAGAAGTTTG TATCAATATA AAAACTCTAA AGTATATAAA	1500
CAAACATTCA ATTAGTGTA ATCATAGCAA GCATATCTTT TCATACGTGT CTAGTTAATT	1560
TAAAGAATTA ATT ATG ACA TTT AGA ATG ACT TCA CTT GTG TTA CTT CTG	1609
Met Thr Phe Arg Met Thr Ser Leu Val Leu Leu Leu	
1 5 10	
CTG CTG AGC ATA GAT TGT ATA GTA AAG TCA GAA ATA ACA AGC GCA CAA	1657
Leu Leu Ser Ile Asp Cys Ile Val Lys Ser Glu Ile Thr Ser Ala Gln	
15 20 25	
ACC CCA AGA TGC TTA GCT GCT AAC AAT AGC TTT CCA CGG TCT GTG ATG	1705
Thr Pro Arg Cys Leu Ala Ala Asn Asn Ser Phe Pro Arg Ser Val Met	
30 35 40	
GTT ACT TTG AGC ATC CGT AAC TGG AAT ACT AGT TCT AAA AGG GCT TCA	1753
Val Thr Leu Ser Ile Arg Asn Trp Asn Thr Ser Ser Lys Arg Ala Ser	
45 50 55 60	
GAC TAC TAC AAT AGA TCT ACG TCT CCT TGG ACT CTC CAT CGC AAT GAA	1801
Asp Tyr Tyr Asn Arg Ser Thr Ser Pro Trp Thr Leu His Arg Asn Glu	
65 70 75	
GAT CAA GAT AGA TAT CCC TCT GTG ATT TGG GAA GCA AAG TGT CGC TAC	1849
Asp Gln Asp Arg Tyr Pro Ser Val Ile Trp Glu Ala Lys Cys Arg Tyr	
80 85 90	
TTA GGA TGT GTT AAT GCT GAT GGG AAT GTA GAC TAC CAC ATG AAC TCA	1897
Leu Gly Cys Val Asn Ala Asp Gly Asn Val Asp Tyr His Met Asn Ser	
95 100 105	
GTC CCT ATC CAA CAA GAG ATT CTA GTG GTG CGC AAA GGG CAT CAA CCC	1945
Val Pro Ile Gln Gln Glu Ile Leu Val Val Arg Lys Gly His Gln Pro	
110 115 120	
TGC CCT AAT TCA TTT AGG CTA GAG AAG ATG CTA GTG ACT GTA GGC TGC	1993
Cys Pro Asn Ser Phe Arg Leu Glu Lys Met Leu Val Thr Val Gly Cys	
125 130 135 140	
ACA TGC GTT ACT CCC ATT GTT CAC AAT GTA GAC TAAAAGCTAT CTAAATTTTG	2046
Thr Cys Val Thr Pro Ile Val His Asn Val Asp	
145 150	
AAAATTAACA TTTCATAAA AAACAAAAAC TTGATTTTTT TCTTTTAAAT AAAAAAGTT	2106
TAATATAAGT TCTGGCTTGT TTGGTTTTTG ACTAATCAAT GTAGATCACA CTTGTGATCT	2166

TAGCTCTCGG GAAGCAATGT AAGAAAATAT ATTTAACTTA AGAGTTTTAG ACTTGCTTGA	2226
GTTTTATGAG TAAAAAACAA AGAATAAGCA CAGCTTCTTG TATCTTCTTT TAAAAACTTT	2286
AAGTTATTTA TGTATTTAAT ATAATCTAAT GTTCTTAAA CATGTTGAGT TTGAGGTCCA	2346
CTAATACAAC ATTATAATTT TTTCTGTTAT AACACTTTTG CAAGAAGAAC TCATTTTATA	2406
GAAAATGAGC AGTATTCAAA AAAAATGTTT GATATGCTGT AATATTGGAG AGGAAGAACT	2466
TTTACAAGCA TGTGATTGTC CTAGCAGAGT CCATCATACA TGCTTACAAA GTCA	2520

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Thr Phe Arg Met Thr Ser Leu Val Leu Leu Leu Leu Ser Ile	1	5	10	15
Asp Cys Ile Val Lys Ser Glu Ile Thr Ser Ala Gln Thr Pro Arg Cys	20	25	30	
Leu Ala Ala Asn Asn Ser Phe Pro Arg Ser Val Met Val Thr Leu Ser	35	40	45	
Ile Arg Asn Trp Asn Thr Ser Ser Lys Arg Ala Ser Asp Tyr Tyr Asn	50	55	60	
Arg Ser Thr Ser Pro Trp Thr Leu His Arg Asn Glu Asp Gln Asp Arg	65	70	75	80
Tyr Pro Ser Val Ile Trp Glu Ala Lys Cys Arg Tyr Leu Gly Cys Val	85	90	95	
Asn Ala Asp Gly Asn Val Asp Tyr His Met Asn Ser Val Pro Ile Gln	100	105	110	
Gln Glu Ile Leu Val Val Arg Lys Gly His Gln Pro Cys Pro Asn Ser	115	120	125	
Phe Arg Leu Glu Lys Met Leu Val Thr Val Gly Cys Thr Cys Val Thr	130	135	140	
Pro Ile Val His Asn Val Asp	145	150		

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..237
- (D) OTHER INFORMATION: /product= "human CTLA-8 fragment"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

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MGC AAT GAG GAC CCT GAG AGA TAT CCC TCT GTG ATC TGG GAG GCA AAG      48
Xaa Asn Glu Asp Pro Glu Arg Tyr Pro Ser Val Ile Trp Glu Ala Lys
  1             5             10             15

TGC CGC CAC TTG GGC TGC ATC AAC GCT GAT GGG AAC GTG GAC TAC CAC      96
Cys Arg His Leu Gly Cys Ile Asn Ala Asp Gly Asn Val Asp Tyr His
          20             25             30

ATG AAC TCT GTC CCC ATC CAG CAA GAG ATC CTG GTC CTG CGC AGG GAG     144
Met Asn Ser Val Pro Ile Gln Gln Glu Ile Leu Val Leu Arg Arg Glu
      35             40             45

CCT CCA CAC TGC CCC AAC TCC TTC CGG CTG GAG AAG ATA CTG GTG TCC     192
Pro Pro His Cys Pro Asn Ser Phe Arg Leu Glu Lys Ile Leu Val Ser
      50             55             60

GTG GGC TGC ACC TGT GTC ACC CCG ATT GTC CAC CAT GTG GCC           234
Val Gly Cys Thr Cys Val Thr Pro Ile Val His His Val Ala
      65             70             75

TAA                                                                237

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(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Ser or Arg"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```

Xaa Asn Glu Asp Pro Glu Arg Tyr Pro Ser Val Ile Trp Glu Ala Lys
  1             5             10             15

```

Cys	Arg	His	Leu	Gly	Cys	Ile	Asn	Ala	Asp	Gly	Asn	Val	Asp	Tyr	His
			20					25					30		
Met	Asn	Ser	Val	Pro	Ile	Gln	Gln	Glu	Ile	Leu	Val	Leu	Arg	Arg	Glu
		35					40					45			
Pro	Pro	His	Cys	Pro	Asn	Ser	Phe	Arg	Leu	Glu	Lys	Ile	Leu	Val	Ser
		50				55					60				
Val	Gly	Cys	Thr	Cys	Val	Thr	Pro	Ile	Val	His	His	Val	Ala		
65						70				75					

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 510 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(11) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..510
(D) OTHER INFORMATION: /note= "full length human CTLA-8 clone"

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 43..510
(D) OTHER INFORMATION: /product="human CTLA-8"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGCACAAACT CATCCATCCC CAGTTGATTG GAAGAAACAA CG ATG ACT CCT GGG															54	
Met Thr Pro Gly																
1																
AAG	ACC	TCA	TTG	GTG	TCA	CTG	CTA	CTG	CTG	CTG	AGC	CTG	GAG	GCC	ATA	102
Lys	Thr	Ser	Leu	Val	Ser	Leu	Leu	Leu	Leu	Leu	Ser	Leu	Glu	Ala	Ile	
5			10			15			20							
GTG	AAG	GCA	GGA	ATC	ACA	ATC	CCA	CGA	AAT	CCA	GGA	TGC	CCA	AAT	TCT	150
Val	Lys	Ala	Gly	Ile	Thr	Ile	Pro	Arg	Asn	Pro	Gly	Cys	Pro	Asn	Ser	
25				30				35								
GAG	GAC	AAG	AAC	TTC	CCC	CGG	ACT	GTG	ATG	GTC	AAC	CTG	AAC	ATC	CAT	198
Glu	Asp	Lys	Asn	Phe	Pro	Arg	Thr	Val	Met	Val	Asn	Leu	Asn	Ile	His	
40				45				50								
AAC	CGG	AAT	ACC	AAT	ACC	AAT	CCC	AAA	AGG	TCC	TCA	GAT	TAC	TAC	AAC	246
Asn	Arg	Asn	Thr	Asn	Thr	Asn	Pro	Lys	Arg	Ser	Ser	Asp	Tyr	Tyr	Asn	
55			60			65										
CGA	TCC	ACC	TCA	CCT	TGG	AAT	CTC	CAC	CGC	AAT	GAG	GAC	CCT	GAG	AGA	294
Arg	Ser	Thr	Ser	Pro	Trp	Asn	Leu	His	Arg	Asn	Glu	Asp	Pro	Glu	Arg	
70			75			80										

TAT CCC TCT GTG ATC TGG GAG GCA AAG TGC CGC CAC TTG GGC TGC ATC	342
Tyr Pro Ser Val Ile Trp Glu Ala Lys Cys Arg His Leu Gly Cys Ile	
85 90 95 100	
AAC GCT GAT GGG AAC GTG GAC TAC CAC ATG AAC TCT GTC CCC ATC CAG	390
Asn Ala Asp Gly Asn Val Asp Tyr His Met Asn Ser Val Pro Ile Gln	
105 110 115	
CAA GAG ATC CTG GTC CTG CGC AGG GAG CCT CCA CAC TGC CCC AAC TCC	438
Gln Glu Ile Leu Val Leu Arg Arg Glu Pro Pro His Cys Pro Asn Ser	
120 125 130	
TTC CGG CTG GAG AAG ATA CTG GTG TCC GTG GGC TGC ACC TGT GTC ACC	486
Phe Arg Leu Glu Lys Ile Leu Val Ser Val Gly Cys Thr Cys Val Thr	
135 140 145	
CCG ATT GTC CAC CAT GTG GCC TAA	510
Pro Ile Val His His Val Ala	
150 155	

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Thr Pro Gly Lys Thr Ser Leu Val Ser Leu Leu Leu Leu Leu Ser	
1 5 10 15	
Leu Glu Ala Ile Val Lys Ala Gly Ile Thr Ile Pro Arg Asn Pro Gly	
20 25 30	
Cys Pro Asn Ser Glu Asp Lys Asn Phe Pro Arg Thr Val Met Val Asn	
35 40 45	
Leu Asn Ile His Asn Arg Asn Thr Asn Thr Asn Pro Lys Arg Ser Ser	
50 55 60	
Asp Tyr Tyr Asn Arg Ser Thr Ser Pro Trp Asn Leu His Arg Asn Glu	
65 70 75 80	
Asp Pro Glu Arg Tyr Pro Ser Val Ile Trp Glu Ala Lys Cys Arg His	
85 90 95	
Leu Gly Cys Ile Asn Ala Asp Gly Asn Val Asp Tyr His Met Asn Ser	
100 105 110	
Val Pro Ile Gln Gln Glu Ile Leu Val Leu Arg Arg Glu Pro Pro His	
115 120 125	
Cys Pro Asn Ser Phe Arg Leu Glu Lys Ile Leu Val Ser Val Gly Cys	
130 135 140	
Thr Cys Val Thr Pro Ile Val His His Val Ala	
145 150 155	

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1134 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1134
- (D) OTHER INFORMATION: /note= "mouse CTLA-8 fragment"

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 45..521
- (D) OTHER INFORMATION: /product= "mouse CTLA-8"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GAGGCTCAAG TGCACCCAGC ACCAGCTGAT CAGGACGCGC AAAC ATG AGT CCA GGG	56
Met Ser Pro Gly	
1	
AGA GCT TCA TCT GTG TCT CTG ATG CTG TTG CTG CTG CTG AGC CTG GCG	104
Arg Ala Ser Ser Val Ser Leu Met Leu Leu Leu Leu Leu Ser Leu Ala	
5 10 15 20	
GCT ACA GTG AAG GCA GCA GCG ATC ATC CCT CAA AGC TCA GCG TGT CCA	152
Ala Thr Val Lys Ala Ala Ala Ile Ile Pro Gln Ser Ser Ala Cys Pro	
25 30 35	
AAC ACT GAG GCC AAG GAC TTC CTC CAG AAT GTG AAG GTC AAC CTC AAA	200
Asn Thr Glu Ala Lys Asp Phe Leu Gln Asn Val Lys Val Asn Leu Lys	
40 45 50	
GTC TTT AAC TCC CTT GGC GCA AAA GTG AGC TCC AGA AGG CCC TCA GAC	248
Val Phe Asn Ser Leu Gly Ala Lys Val Ser Ser Arg Arg Pro Ser Asp	
55 60 65	
TAC CTC AAC CGT TCC ACG TCA CCC TGG ACT CTC CAC CGC AAT GAA GAC	296
Tyr Leu Asn Arg Ser Thr Ser Pro Trp Thr Leu His Arg Asn Glu Asp	
70 75 80	
CCT GAT AGA TAT CCC TCT GTG ATC TGG GAA GCT CAG TGC CGC CAC CAG	344
Pro Asp Arg Tyr Pro Ser Val Ile Trp Glu Ala Gln Cys Arg His Gln	
85 90 95 100	
CGC TGT GTC AAT GCG GAG GGA AAG CTG GAC CAC CAC ATG AAT TCT GTT	392
Arg Cys Val Asn Ala Glu Gly Lys Leu Asp His His Met Asn Ser Val	
105 110 115	
CTC ATC CAG CAA GAG ATC CTG GTC CTG AAG AGG GAG CCT GAG AGC TGC	440
Leu Ile Gln Gln Glu Ile Leu Val Leu Lys Arg Glu Pro Glu Ser Cys	
120 125 130	

CCC TTC ACT TTC AGG GTC GAG AAG ATG CTG GTG GGT GTG GGC TGC ACC 488
 Pro Phe Thr Phe Arg Val Glu Lys Met Leu Val Gly Val Gly Cys Thr
 135 140 145

TGC GTG GCC TCG ATT GTC CGC CAG GCA GCC TAAACAGAGA CCCGCGGCTG 538
 Cys Val Ala Ser Ile Val Arg Gln Ala Ala
 150 155

ACCCCTAAGA AACCCCCACG TTTCTCAGCA AACTTACTTG CATTTTAAAC ACAGTTCGTG 598

CTATTGATTT TCAGCAAGGA ATGTGGATTC AGAGGCAGAT TCAGAATTGT CTGCCCTCCA 658

CAATGAAAAG AAGGTGTAAA GGGGTCCCAA ACTGCTTCGT GTTTGTTTTT CTGTGGACTT 718

TAAATTATTT GTGTATTTAC AATATCCCAA GATAACTTTG AAGGCGTAAC TTATTTAATG 778

AAGTATCTAC ATTATTATTA TGTTTCTTTC TGAAGAAGAC AAAATTCAAG ACTCAGAAAT 838

TTTATTATTT AAAAGGTAAG CCTATATTTA TATGAGCTAT TTATGAATCT ATTTATTTTT 898

CTTCAGTATT TGAAGTATTA AGAACATGAT TTTCAGATCT ACCTAGGGAA GTCCTAACTA 958

AGATTAAATA TTAATGGAAA TTTCAGCTTT ACTATTTGGT TGATTTAAGG TTCTCTCCTC 1018

TGAATGGGGT GAAAACCAAA CTTAGTTTTA TGTTTAATAA CTTTTTAAAT TATTGAAGAT 1078

TCAAAAAAATT GGATAATTTA GCTCCCTACT CTGTTTTTAA AAAAAAAAAA AAAAAA 1134

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Ser Pro Gly Arg Ala Ser Ser Val Ser Leu Met Leu Leu Leu Leu
 1 5 10 15

Leu Ser Leu Ala Ala Thr Val Lys Ala Ala Ala Ile Ile Pro Gln Ser
 20 25 30

Ser Ala Cys Pro Asn Thr Glu Ala Lys Asp Phe Leu Gln Asn Val Lys
 35 40 45

Val Asn Leu Lys Val Phe Asn Ser Leu Gly Ala Lys Val Ser Ser Arg
 50 55 60

Arg Pro Ser Asp Tyr Leu Asn Arg Ser Thr Ser Pro Trp Thr Leu His
 65 70 75 80

Arg Asn Glu Asp Pro Asp Arg Tyr Pro Ser Val Ile Trp Glu Ala Gln
 85 90 95

Cys Arg His Gln Arg Cys Val Asn Ala Glu Gly Lys Leu Asp His His
 100 105 110

Met Asn Ser Val Leu Ile Gln Gln Glu Ile Leu Val Leu Lys Arg Glu
115 120 125

Pro Glu Ser Cys Pro Phe Thr Phe Arg Val Glu Lys Met Leu Val Gly
130 135 140

Val Gly Cys Thr Cys Val Ala Ser Ile Val Arg Gln Ala Ala
145 150 155